What is claimed is:

1. A method for genetically identifying an animal with respect to its potential to reproductive longevity comprising:

obtaining a sample of genetic material from an animal; and

assaying for the presence of a polymorphism in the insulin-like growth factor 1 receptor gene (IGF-1R), wherein the polymorphism is associated with reproductive longevity.

2. The method of claim 1 wherein said polymorphism is selected from the group consisting of: a single nucleotide polymorphism (SNP), a deletion, and an insertion.

3. The method of claim 1 wherein the animal is selected from a group consisting of: a mouse ,a pig, and a cow.

4. The method of claim 1 wherein a step of assaying the polymorphism is selected from the group consisting of: direct sequencing, restriction fragment length polymorphism (RFLP) analysis, single-stranded conformation polymorphism (SSCP), PCR amplification of specific alleles, amplification of DNA target by PCR followed by a mini-sequencing assay, allelic discrimination during PCR, Genetic Bit Analysis, Pyrosequencing, oligonucleotide ligation assay, and analysis of melting curves.

5. The method of claim 4 wherein the step of assaying the polymorphism is RFLP.

6. The method of claim 4 wherein the step of assaying the polymorphism is SSCP.

7. The method of claim 1 wherein the step of assaying for the presence of the polymorphism comprises the steps of:

digesting the genetic material with a restriction endonuclease that cleaves the gene in at least one place, wherein a particular restriction endonuclease pattern indicates the presence or absence of a polymorphism;

separating the fragments obtained from the digestion;

detecting a restriction pattern generated by the fragments; and

comparing the pattern with a second restriction pattern for the gene obtained by using the restriction endonuclease, wherein the second restriction pattern is associated with reproductive longevity.

8. The method of claim 7 wherein said separation is by gel electrophoresis.

9. The method of claim 7 further comprising:

amplifying the gene or a portion thereof which contains at least one polymorphism, prior to digestion.

10. The method of claim 9 wherein the amplification includes selecting a forward and a reverse sequence primer capable of amplifying a region of the gene which contains a polymorphism.

11. The method of claim 1 wherein the polymorphism is identified as an A to G nucleotide substitution at position 3876 of the gene.

12. The method of claim 1 wherein the polymorphism is identified as a G to A nucleotide substitution at position 331 of the gene.

13. The method of claim 1 wherein the polymorphism is a 12 base pair deletion at positions 3896-3907 of the gene.

14. The method of claim 7 wherein the restriction endonuclease is *HpaII*.

15. The method of claim 7 wherein the restriction endonuclease *DpnII*.

16. The method of claim 7 wherein the restriction endonuclease is *TaqI*.

17. The method of claim 7 wherein the restriction endonuclease is *MnlI*.

18. The method of claim 7 wherein the restriction endonuclease is *AvaII*.

19. The method of claim 10 wherein the forward primer is SEQ ID NO:8 and wherein the reverse primer is SEQ ID NO:9.

20. The method of claim 10 wherein the forward primer is SEQ ID NO:10 and wherein the reverse primer is SEQ ID NO:11.

21. The method of claim 10 wherein the forward primer is SEQ ID NO:12 and wherein the reverse primer is SEQ ID NO:13.

22. The method of claim 10 wherein the forward primer is SEQ ID NO:14 and wherein the reverse primer is SEQ ID NO:15.

23. The method of claim 10 wherein the forward primer is SEQ ID NO:16 and wherein the reverse primer is SEQ ID NO:17.

24. The method of claim 10 wherein the forward primer is SEQ ID NO:18 and wherein the reverse primer is SEQ ID NO:19.

25. A method of screening animals to determine those more likely to have reproductive longevity, the method comprising:

obtaining a biological sample from an animal; and

assaying for the presence of a genotype in the IGF-1R gene, wherein the genotype is associated with reproductive longevity and characterized by a restriction fragment pattern, wherein said pattern when compared to a second restriction pattern is known to have or not have a desired polymorphic marker, the presence of said marker being indicative of an animal more likely to have reproductive longevity.

26. The method of claim 25 wherein the assaying step comprises amplifying the gene or a region thereof containing the marker with a forward and a reverse sequence primer.

27. The method of claim 26 wherein the forward primer is SEQ ID NO:8 and the reverse primer is SEQ ID NO:9.

28. The method of claim 26 wherein the forward primer is SEQ ID NO:10 and the reverse primer is SEQ ID NO:11.

29. The method of claim 26 wherein the forward primer is SEQ ID NO:12 and said reverse primer is SEQ ID NO:13.

30. The method of claim 26 wherein the forward primer is SEQ ID NO:14 and the reverse primer is SEQ ID NO:15.

31. The method of claim 26 wherein the forward primer is SEQ ID NO:16 and the reverse primer is SEQ ID NO:17.

32. The method of claim 26 wherein the forward primer is SEQ ID NO:18 and the reverse primer is SEQ ID NO:19.

33. The method of claim 25 wherein the marker is *DpnII*.

34. The method of claim 25 wherein the marker is *HpaII*.

35. The method of claim 25 wherein the marker is *TaqI*.

36. The method of claim 25 wherein the marker is *Mn1I*.

37. The method of claim 25 wherein the marker is *AvaII*.

38. The method of claim 33 wherein a G to A nucleotide substitution results in a restriction pattern characterized by a 328 nucleotide fragment, a 125 nucleotide fragment, and a 32 nucleotide fragment.

39. The method of claim 34 wherein an A to G nucleotide substitution results in a restriction pattern characterized by a 373 nucleotide fragment, a 134 nucleotide fragment, and a 127 nucleotide fragment.

40. The method of claim 34 wherein the deletion is characterized by a 12 bp fragment having SEQ ID NO:20 appearing once in the IGF-1R gene.

41. The method of claim 35 wherein a G to A nucleotide substitution results in a restriction pattern characterized by a 135 nucleotide fragment and an 84 nucleotide fragment.

42. The method of claim 36 wherein an G to C nucleotide substitution results in a restriction pattern characterized by a 137 nucleotide fragment, a 104 nucleotide fragment, a 55 nucleotide fragment, and an 11 nucleotide fragment.

43. The method of claim 37 wherein an G to A nucleotide substitution results in a restriction pattern characterized by a 122 nucleotide fragment, an 81 nucleotide fragment, a 60 nucleotide fragment, and a 44 nucleotide fragment.

44. The method of claim 25 wherein said animal is selected from the group consisting of: a pig and a mouse.

45. A method for screening animals to determine those more likely to exhibit favorable traits associated with reproductive longevity, said method comprising:
obtaining a genetic sample from an animal; and
detecting the presence or absence of at least one allele in the IGF-1R gene wherein the presence of the allele is predictive of the animal having reproductive longevity.

46. The method of claim 45 wherein the allele is defined in intron 16 of the gene.

47. The method of claim 45 wherein the allele is defined in exon 21 at position 3876 of the gene.

48. The method of claim 45 wherein the allele is defined in exon 21 at positions 3896-3907 of the gene.

49. The method of claim 45 wherein the allele is defined at position 27 at the end of intron 16 of the gene.

50. The method of claim 45 wherein the allele is defined at position 73 at the end of intron 16 of the gene.

51. The method of claim 45 wherein the animal is selected from a group consisting of: a pig and a mouse.

52. A method for determining the haplotype of the IGF-1R gene of an animal comprising:

obtaining a genetic sample from an animal; and

analyzing the genetic sample for the presence of an IGF-1R gene A_1D_1, A_1D_2, or A_2D_1 haplotype allele, wherein the haplotype effects reproductive performance or the ability to sustain stress factors.

53. The method of claim 52 wherein the A_1D_1 allele is indicative of having a favorable effect on lactation and pregnancy stress.

54. The method of claim 52 wherein the A_1D_2 allele is indicative of having a negative effect on reproductive performance.

55. The method of claim 52 wherein the A_2D_1 allele is indicative of reproductive longevity.

56. The method of claim 52 wherein the animal is a mouse.

57. A method for genotyping an animal for reproductive longevity, the method comprising:

obtaining a sample of genetic material from an animal;

detecting a polymorphism in the IGF-1R gene of the animal;

determining whether the animal possesses a marker, wherein the marker is indicative of the animal having two copies of allele 2.

58. The method of claim 57 wherein the step of detecting the polymorphism comprises:

digesting amplified nucleic acid with a restriction enzyme; and

separating the nucleic acid fragments according to size such that a restriction fragment pattern is generated,

wherein the restriction fragment pattern generated is indicative of an animal reproductive longevity.

59. The method of claim 57 wherein prior to digesting the nucleic acid with a restriction enzyme, amplifying the nucleic acid with a forward primer and a reverse primer.

60. The method of claim 59 wherein the forward and reverse primer is SEQ ID NO:21 and SEQ ID NO:22.

61. The method of claim 57 wherein the restriction enzyme is *FokI*.

62. The method of claim 58 wherein the restriction pattern characterized by a 295 nucleotide fragment, and a 55 nucleotide fragment.

63. The method of claim 57 wherein the marker is positively associated with longevity.

64. The method of claim 57 wherein the animal is a pig.

65. A method for genetically identifying an animal comprising:
obtaining a sample of genetic material from an animal; and
assaying for the presence of a genotype in the IGF-1R gene sequence as set forth in SEQ ID NO:1 or a region thereof in the sample,
wherein the animal possesses a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:1 or a fragment thereof.

66. The method of claim 65 wherein the polymorphism is identified by a G to A nucleotide substitution in intron 16.

67. The method of claim 65 wherein the polymorphism is identified by an A to G nucleotide substitution in exon 21.

68. The method of claim 65 wherein the polymorphism is identified as a 12 bp deletion in exon 21.

69. The method of claim 65 wherein the polymorphism is identified as an insertion of a G nucleotide in intron 16 at position 176.

70. The method of claim 65 wherein the animal is a mouse.

71. A method for genetically identifying an animal comprising:
obtaining a sample of genetic material from an animal; and
assaying for the presence of a genotype in the IGF-1R gene sequence as set forth in SEQ ID NO:7 or a region thereof in the sample,
wherein the animal posses a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:7 or a fragment thereof.

72. The method of claim 71 wherein said polymorphism is identified as a G to A nucleotide substitution in intron 16.

73. The method of claim 71 wherein said polymorphism is identified as a G to C nucleotide substitution in intron 16.

74. The method of claim 71 wherein said polymorphism is identified as a G to A nucleotide substitution in exon 8.

75. The method of claim 71 wherein the animal is a pig.

76. The method of claim 65 wherein the polymorphism is an A to G nucleotide substitution in exon 21 at position 3876.

77. The method of claim 65 wherein the polymorphism is a 12 bp deletion in exon 21 at positions 3896-3907.

78. The method of claim 71 wherein said polymorphism is a G to A nucleotide substitution at position 27 from the end of intron 16.

79. The method of claim 71 wherein said polymorphism is a G to C nucleotide substitution at position 73 from the end of intron 16.

80. A method for genetically identifying cattle with respect to its potential to reproductive longevity comprising:
obtaining a sample of genetic material from a cow; and
assaying for the presence of a polymorphism in the insulin-like growth factor 1 receptor gene (IGF-1R), wherein the polymorphism is associated with reproductive longevity.